High-throughput epitope identification for snakebite antivenom

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High-throughput epitope identification for snakebite antivenom

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Introduction

Insight into the epitopic recognition pattern for polyclonal antivenoms is a strong tool for accurate prediction of antivenom cross-reactivity and provides a basis for design of novel antivenoms. In this work, a high-throughput approach was applied to characterize linear epitopes in 966 individual antivenoms from 110 species of pit vipers (Crotalidae) using the ICP Crotalidae antivenom. Due to an abundance of snake venom metalloproteinases and phospholipase A₂, in the venoms used for production of the investigated antivenom, this study focuses on these toxin families.

Objectives

• Identify epitopes in toxins used in immunization
• Characterize tolerated amino acid substitutions in identified epitopes
• Predict cross-reactivity of antivenom

Epitopes locate to surface regions

To identify epitopes, the observed peptide specific signal intensities were mapped back to the amino acid sequence of each peptide. For two or more overlapping 15-mer peptides with median signals above 20 AU, epitope core sequences were localized and subsequently mapped to crystal structures or homology models. As examples, P-I metalloproteinase and lys49-phospholipase A₂ from Bothrops asper (venom used in antivenom production) are presented here.

Studying linear epitopes using peptide microarrays

To identify epitopes in toxins specific signal intensities were mapped back to the amino acid sequence of each peptide. For two or more overlapping 15-mer peptides with median signals above 20 AU, epitope core sequences were localized and subsequently mapped to crystal structures or homology models. As examples, P-I metalloproteinase and lys49-phospholipase A₂ from Bothrops asper (venom used in antivenom production) are presented here.

Effect on cross-recognition

The μ-helical red epitope in the B. asper metalloproteinase is found to be highly conserved among pit viper metalloproteinases. Based on multiple sequence alignment of pit viper toxins sharing at least seven of the eight 15-mer peptides harboring the epitope, we find that the epitopes are small effect on antivenom recognition. Expanding the analysis to the 42 toxins that share at least five of the epitope residues, binding is still observed in all of the corresponding eight 15-mer peptides, although the microarray signals are reduced up to seven times (data not shown).

Conclusions

• Custom-designed high density peptide microarray technology enables parallel automated identification of epitopes in hundreds of toxins.
• Integrating multiple sequence alignment allows investigation of the effect of epitope variation on antivenom recognition.
• Cross-reactivity of antivenom is correlated to the degree of conservation in toxin epitopes and flanking residues.

References


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